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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/393,023

DATE: 10/21/1999
TIME: 15:32:10

INPUT SET: S33730.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Meissner, Paul S.
Coleman, Timothy A.

(ii) TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STEWART & OLSTEIN

(B) STREET: 6 Becker Farm Road

(C) CITY: Roseland

(D) STATE: N.J.

(E) COUNTRY: U.S.A

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/393,023

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/471,371

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ferraro, Gregory D.

(B) REGISTRATION NUMBER: 36,134

(C) REFERENCE/DOCKET NUMBER: 32580-455

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (201) 994-1700

(B) TELEFAX: (201) 994-1744

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47 (2) INFORMATION FOR SEQ ID NO:1:
48
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 774 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: single
53 (D) TOPOLOGY: linear
54
55 (ii) MOLECULE TYPE: cDNA
56
57
58 (ix) FEATURE:
59 (A) NAME/KEY: CDS
60 (B) LOCATION: 82..771
61
62
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65 ATGCAGAAGA CTCTTCAAGA TTCAGCTTTC CTGGAAACTG ATCTTCAATG CACTAAGAGA 60
66
67 AGGAGACTCT CAAACCCAAA A ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG 111
68 Met Thr Trp Arg His His Val Arg Leu Leu
69 1 5 10
70
71 TTT ACG GTC AGT TTG GCA TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT 159
72 Phe Thr Val Ser Leu Ala Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr
73 15 20 25
74
75 CAA AGA GAG AAA CAT AAC GGC GGT AGA GAG GAA GTC ACC AAG GTT GCC 207
76 Gln Arg Glu Lys His Asn Gly Gly Arg Glu Glu Val Thr Lys Val Ala
77 30 35 40
78
79 ACT CAG AAG CAC CGA CAG TCA CCG CTC AAC TGG ACC TCC AGT CAT TTC 255
80 Thr Gln Lys His Arg Gln Ser Pro Leu Asn Trp Thr Ser Ser His Phe
81 45 50 55
82
83 GGA GAG GTG ACT GGG AGC GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC 303
84 Gly Glu Val Thr Gly Ser Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu
85 60 65 70
86
87 CCC TAC TCC CGG GCT TTC GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC 351
88 Pro Tyr Ser Arg Ala Phe Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys
89 75 80 85 90
90
91 TGC AGG AAC GGC GGT ACC TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG 399
92 Cys Arg Asn Gly Gly Thr Cys Val Leu Gly Ser Phe Cys Val Cys Pro
93 95 100 105
94
95 GCC CAC TTC ACC GGC CGC TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA 447
96 Ala His Phe Thr Gly Arg Tyr Cys Glu His Asp Gln Arg Arg Ser Glu
97 110 115 120
98
99 TGC GGC GCC CTG GAG CAC GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC 495

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100 Cys Gly Ala Leu Glu His Gly Ala Trp Thr Leu Arg Ala Cys His Leu
101           125                      130                      135
102
103 TGC AGG TGC ATC TTC GGG GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT      543
104 Cys Arg Cys Ile Phe Gly Ala Leu His Cys Leu Pro Leu Gln Thr Pro
105           140                      145                      150
106
107 GAC CGC TGT GAC CCG AAA GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG      591
108 Asp Arg Cys Asp Pro Lys Asp Phe Leu Ala Ser His Ala His Gly Pro
109           155                      160                      165                      170
110
111 AGC GCC GGG GGC GCG CCC AGC CTG CTA CTC TTG CTG CCC TGC GCA ACT      639
112 Ser Ala Gly Gly Ala Pro Ser Leu Leu Leu Leu Leu Pro Cys Ala Thr
113           175                      180                      185
114
115 CCT GCA CCG GCC TCC TGC GCC CGG ATG CGC CCG CGC ACC CTC GGT CCC      687
116 Pro Ala Pro Ala Ser Cys Ala Arg Met Arg Pro Arg Thr Leu Gly Pro
117           190                      195                      200
118
119 TGG TCC CTT CCG TCC TCC AGC GGG AGC GGC GCC CCT GCG GAA GGC CGG      735
120 Trp Ser Leu Pro Ser Ser Ser Gly Ser Gly Ala Pro Ala Glu Gly Arg
121           205                      210                      215
122
123 GAC TTG GGC ATC GCC TTT AAT TTT CTA TGT TGT AAA TAA      774
124 Asp Leu Gly Ile Ala Phe Asn Phe Leu Cys Cys Lys
125           220                      225                      230
126
127
128 (2) INFORMATION FOR SEQ ID NO:2:
129
130 (i) SEQUENCE CHARACTERISTICS:
131 (A) LENGTH: 230 amino acids
132 (B) TYPE: amino acid
133 (D) TOPOLOGY: linear
134
135 (ii) MOLECULE TYPE: protein
136
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
138
139 Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
140   1           5           10           15
141
142 Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
143           20           25           30
144
145 Gly Gly Arg Glu Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
146           35           40           45
147
148 Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
149           50           55           60
150
151 Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
152           65           70           75           80

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153
154 Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
155 85 90 95
156
157 Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
158 100 105 110
159
160 Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
161 115 120 125
162
163 Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
164 130 135 140
165
166 Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
167 145 150 155 160
168
169 Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
170 165 170 175
171
172 Ser Leu Leu Leu Leu Leu Pro Cys Ala Thr Pro Ala Pro Ala Ser Cys
173 180 185 190
174
175 Ala Arg Met Arg Pro Arg Thr Leu Gly Pro Trp Ser Leu Pro Ser Ser
176 195 200 205
177
178 Ser Gly Ser Gly Ala Pro Ala Glu Gly Arg Asp Leu Gly Ile Ala Phe
179 210 215 220
180
181 Asn Phe Leu Cys Cys Lys
182 225 230
183
184 (2) INFORMATION FOR SEQ ID NO:3:
185
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 36 base pairs
188 (B) TYPE: nucleic acid
189 (C) STRANDEDNESS: single
190 (D) TOPOLOGY: linear
191
192 (ii) MOLECULE TYPE: other nucleic acid
193 (A) DESCRIPTION: /desc = "PRIMER"
194
195
196
197
198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
199
200 ACTCTTGGAT CCAATTTGGG AAACAGCTAT CAAAGA
201
202 (2) INFORMATION FOR SEQ ID NO:4:
203
204 (i) SEQUENCE CHARACTERISTICS:
205 (A) LENGTH: 42 base pairs

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206 (B) TYPE: nucleic acid
207 (C) STRANDEDNESS: single
208 (D) TOPOLOGY: linear
209
210 (ii) MOLECULE TYPE: other nucleic acid
211 (A) DESCRIPTION: /desc = "PRIMER"
212
213
214
215
216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
217
218 TACAACCTCTA GACTATTATT TACAACATAG AAAATTAAAG GC
219
220 (2) INFORMATION FOR SEQ ID NO:5:
221
222 (i) SEQUENCE CHARACTERISTICS:
223 (A) LENGTH: 36 base pairs
224 (B) TYPE: nucleic acid
225 (C) STRANDEDNESS: single
226 (D) TOPOLOGY: linear
227
228 (ii) MOLECULE TYPE: other nucleic acid
229 (A) DESCRIPTION: /desc = "PRIMER"
230
231
232
233
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
235
236 ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT
237
238 (2) INFORMATION FOR SEQ ID NO:6:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 30 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: single
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: other nucleic acid
247 (A) DESCRIPTION: /desc = "PRIMER"
248
249
250
25

42

36

252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 253
 254 TACAACCAGC TGCTATTATT TACAACATAG
 255
 256 (2) INFORMATION FOR SEQ ID NO:7:
 257
 258 (i) SEQUENCE CHARACTERISTICS:

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SEQUENCE VERIFICATION REPORT
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SEQUENCE MISSING ITEM REPORT
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SEQUENCE CORRECTION REPORT
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Original Text

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